



## Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

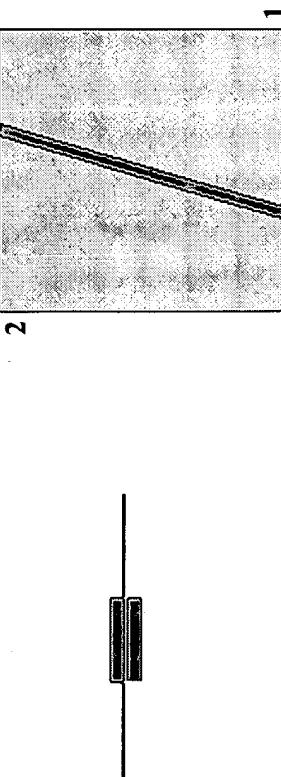
卷之三

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.10 [Oct-19-2004]

Match: [1] Mismatch: [2] gap open: [5] gap extension: [2]  
expect: [10.000] wordsize: [11] Filter  Align

Sequence 1 lcl|seq 1 Length 8509 (1 .. 8509)

Sequence 2 lcl|seq\_2 Length 2517 (1 .. 2517)



**NOTE:** The statistics (bitscore and expect value) is calculated based on the size of nr database

**NOTE:** If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

Score = 4813 bits (2503), Expect = 0.0  
Identities = 2510/2517 (99%)  
Strand = Plus / Plus

```

Query: 2955 ggcaatggtcgaaattcatagaattttgttgggtcgtagggctctgacaggggtg 3014
        ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |
Sbjct: 1 ggcaatggtcgaaattcatagaattttgttgggtcgtagggctctgacaggggtg 60
        ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |

```

Query: 3015 ctgcqqagatctctggctcaacgttagccqcaataatggaaqggttaqtqccccctq 3074

## Blast Result

Page 2 of 7

Sbjct: 61 ||||||| ctgcgggagatctctggctcaggtagggcacaatggaggtttagttggcccttg 120  
Query: 3075 tatcgctctcgctggcattggcatctggccggacatatgtatattccgcttagag 3134  
Sbjct: 121 tatcgctctcgctggcattggcatctggccatgtatattccgcttagag 180  
  
Query: 3135 gattactgatgttctgcctgtcgccgttgtcgccgttgtcggtttgtcggttgtgc 3194  
Sbjct: 181 gattactgatgttctgcctgtcgccgttgtcggtttgtcggttgtgc 240  
  
Query: 3195 ggccctgtccctttgtcccgccctgtccctcaacttttcaacaatcaaaaaatggcgaaagc 3254  
Sbjct: 241 ggccctgtccctttgtcccgccctgtccctcaacttttcaacaatcaaaaaatggcgaaagc 300  
  
Query: 3255 ccttcgttctatagtcttatacgtccaaattacacataatttatcaatagctt 3314  
Sbjct: 301 ccttcgttctatagtcttatacgtccaaattacacataatttatcaatagctt 360  
  
Query: 3315 attcgcttaaaaggagaattggcccaaaaggagtaattggccgatatcggttgttacatggggaggaatcc 3374  
Sbjct: 361 attggcccaaaaggagaattggcccaaaaggagtaattggccgatatcggttgttacatggggaggaatcc 420  
  
Query: 3375 attggcccaaaaggagaattggcccaaaaggagtaattggccgatatcggttgttacatggggaggaatcc 3434  
Sbjct: 421 attggcccaaaaggagaattggcccaaaaggagtaattggccgatatcggttgttacatggggaggaatcc 480  
  
Query: 3435 ccttaatcatttctccccatggaaagacacaatggccgatatcggttgttacatggggaggaatcc 3494  
Sbjct: 481 ccttaatcatttctccccatggaaagacacaatggccgatatcggttgttacatggggaggaatcc 540  
  
Query: 3495 cagacaaaactgtgtccctggcagggtggcagacgggttatatgcgcaatccggcc 3554  
Sbjct: 541 cagacaaaactgtgtccctggcagggtggcagacgggttatatgcgcaatccggcc 600

Query :	3555	cgccgtcaggcgctcaagtcattaaatgataccactgcggccatggct	3614
Sbjct :	601	cgccgtcaggcgctcaagtcattaaatgataccactgcggccatggct	660

Query:	3615	gatgatgtgcgccatgaaatgcggctggccgcattcgcgcataatcgacggcatgaaaaac	3674
Sbjct:	661	gatgatgtgcgccatgaaatgcggctggccgcattcgcgcataatcgacggcatgaaaaac	720

Query: 3675 catgacgcgtgagaaaggccctgaccggcgttgtcaggaggacttagccgcgtcggtgttgcacct 3734  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Shift: 721 catgacgcgtgagaaaggccctgaccggcgttgtcaggaggacttagccgcgtcggtgttgcacct 780

Query: 3795- taccgcaggaggcaaggcggaactcccttagtggaccttcggatcatccgt 3854  
|||||||

Query: 3855 cgtatggcgccggaggactcgaaaccactggggccattctcgaccgtcaaacggtatccatc 3914

Query: 3975 atgagcgcggaaaaccttacgtcccgaggatgcggcgctccttggagtgccggaa 4034

Query: 4095 aaccattttatcgctgtacatggcaaaaggccgaccaaaggccgaaaaatggccgttagcgtggca 4154  
Sbjct: 1141 aaccattttatcgctgtacatggcaaaaggccgaccaaaggccgaaaaatggccgttagcgtggca 1200

Query: 4155 agtgtgactataaggctggaaaggacgacccaaaccgtcgccaggccgagactggcg 4214  
Sbjct: 1201 agtgtgactataaggctggaaaggacgacccaaaccgtcgccaggccgagactggcg 1260

Query: 4215 ggttccaaggtcggtcgagatgctcgccaggggcggaaacgataggcccccctcc 4274  
Sbjct: 1261 ggttccaaggtcggtcgagatgctcgccaggggcggaaacgataggcccccctcc 1320

Query: 4275 ttccccagaaggccggatcacccatcacgtccacacgtggctggagctgaaaacgcctctgtctgt 4334  
Sbjct: 1321 ttccccagaaggccggatcacccatcacgtccacacgtggctggagctgaaaacgcctctgtctgt 1380

Query: 4335 ggcaagcaacaaggacaacgtctgtggacgtcgaaacacatcgaaaaactgttttagatttcgtcgccaaaggta 4394  
Sbjct: 1381 ggcaagcaacaaggacaacgtctgtggacgtcgaaacacatcgaaaaactgttttagatttcgtcgccaaaggta 1440

Query: 4395 ggctggcgctctgtggacgtcgaaacacatcgaaaaactgttttagatttcgtcgccaaaggta 4454  
Sbjct: 1441 ggctggcgctctgtggacgtcgaaacacatcgaaaaactgttttagatttcgtcgccaaaggta 1500

Query: 4455 ggaaaggtttgagtttggagtttccacggcaatagtgttaatgtactttcgtaaaacgg 4514  
Sbjct: 1501 ggaaaggtttgagtttggagtttccacggcaatagtgttaatgtactttcgtaaaacgg 1560

Query: 4515 atgtgcaatatacggttaaaggactatgaaaatcacggctggacaggctgcaaaacgg 4574  
Sbjct: 1561 atgtgcaatatacggttaaaggactatgaaaatcacggctggacaggctgcaaaacgg 1620

Query: 4575 gtgtggccgaccgcacccatcactcgccggctaaaaaggcgtaaaatttccggtaaaaaag 4634  
Sbjct: 1621 gtgtggccgaccgcacccatcactcgccggctaaaaaggcgtaaaatttccggtaaaaaag 1680

Query: 4635 atgaatctggcatgggtatacatccgtcagaattgcacaggtttccatt 4694  
Sbjct: 1681 atgaatctggcatgggtatacatccgtcagaattgcacaggtttccatt 1740

Query: 4695 caaagaaatacaccctaacaacgcaagtatgttaaggcgatgaaaacatg 4754  
Sbjct: 1741 caaagaaatacaccctaacaacgcaagtatgttaaggcgatgaaaacatg 1800

Query: 4755 aaatgacccatggaaatcagcgcatttagagcggtgaaggtcggacttacgcgtatgtttat 4814  
Sbjct: 1801 aaatgacccatggaaatcagcgcatttagagcggtgaaggtcggacttacgcgtatgtttat 1860

Query: 4815 ctgatgccaggaggatcgcgacatggccgcacatggccggacatggccgtcttcaatttcatt 4874  
Sbjct: 1861 ctgatgccaggaggatcgcgacatggccgcacatggccggacatggccgtcttcaatttcatt 1920

Query: 4875 caccgtatggaaagaccggcccccctaaaaaacaatggggaaatggggatatttcattgtat 4934  
Sbjct: 1921 caccgtatggaaagaccggcccccctaaaaaacaatggggaaatggggatatttcattgtat 1980

Query: 4935 cctgggcttcaggagccttgccttaaaacctgtaaatcagccattcttagcgtgtgtataag 4994  
Sbjct: 1981 cctgggcttcaggagccttgccttaaaacctgtaaatcagccattcttagcgtgtgtataag 2040

Query: 4995 aagtaaatatagccacaatagggccatttcattcacatcgtgtgtat 5054  
Sbjct: 2041 aagtaaatatagccacaatagggccatttcattcacatcgtgtgtat 2100

Query: 5055 caatatcaaggatttcatcaatggggaaatttacatgtatcacaggatcatca 5114  
Sbjct: 2101 caatatcaaggatttcatcaatggggaaatttacatgtatcacaggatcatca 2160

Query: 5115 caggatttgttttgttcaatggccctaaaggatt 5174  
Sbjct: 2161 caggatttgttttgttcaatggccctaaaggatt 2220

Sbjct: 2161 caggcatttttttgtatttctaagtgctaacaataactatcgctggccctaaagaaggatt 2220

Query: 5175 gtactattgcgttatctcaccttggttcagaccgataattacagcttgcgaaggccg 5234  
Sbjct: 2221 gtactattgcgttatctcaccttggttcagaccgataattacagcttgcgaaggccg 2280

Query: 5235 gnnnnnnncaggagacacgtttttgtgttaataaactgtctacgttatctcatg 5294  
Sbjct: 2281 gtttttttgcaggagacacgtttttgtgttaataaactgtctacgttatctcatg 2340

Query: 5295 atggtaacatacagcatcatccggggcaacacacccattgtgaatggatattatg 5354  
Sbjct: 2341 atggtaacatacagcatcatccggggcaacacacccattgtgaatggatattatg 2400

Query: 5355 gccccagaaggactggggaaaaacgcgatattgaggcacacggccgcacttttagggccgg 5414  
Sbjct: 2401 gccccagaaggactggggaaaaacgcgatattgaggcacacggccgcacttttagggccgg 2460

Query: 5415 aaggcctataacgtacccaaaacactagaaggccagatttgaggaaaatagggaaacgtg 5471  
Sbjct: 2461 aaggcctataacgtacccaaaacactagaaggccagatttgaggaaaatagggaaacgtg 2517

CPU time: 0.07 user secs. 0.01 sys. secs 0.08 total secs.

Lambda	K	H	
1.33	0.621	1.12	

Gapped Lambda	K	H	
1.33	0.621	1.12	

Matrix: blastn matrix:1 -2  
Gap Penalties: Existence: 5, Extension: 2  
Number of Sequences: 1  
Number of Hits to DB: 908  
Number of extensions: 21  
Number of successful extensions: 14  
Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1  
Number of HSP's gapped: 2  
Number of HSP's successfully gapped: 1  
Number of extra gapped extensions for HSPs above 10.0: 0  
Length of query: 8509  
Length of database: 12,527,565,053  
Length adjustment: 28  
Effective length of query: 8481  
Effective length of database: 12,527,565,025  
Effective search space: 106246278977025  
Effective search space used: 106246278977025  
Neighboring words threshold: 0  
Window for multiple hits: 0  
X1: 11 (21.1 bits)  
X2: 26 (50.0 bits)  
X3: 26 (50.0 bits)  
S1: 12 (23.8 bits)  
S2: 23 (44.9 bits)